

SEQUENCE LISTING

<110> KEITH, TIM
 LITTLE, RANDALL D.
 EERDEWEGH, PAUL VAN
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 ALLEN, KRISTINA
 PANDIT, SUNIL

<120> NOVEL HUMAN GENES RELATING TO RESPIRATORY DISEASES AND OBESITY

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<151> 2000-06-14

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ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro	623
195 200 205	
cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu	671
210 215 220	
tcc agg agg gga cac ccg gtt cac gag ctg ccc acg tcc tct cca gga Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly	719
225 230 235	
ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr	767
240 245 250 255	
ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser	815
260 265 270	

Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg
 65 70 75 80

Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr
 85 90 95

Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 100 105 110

His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro
 115 120 125

Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln
 130 135 140

Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp
 145 150 155 160

Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser
 165 170 175

Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
 180 185 190

Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
 195 200 205

Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
 210 215 220

Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
 225 230 235 240

Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro
 245 250 255

Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr
 260 265 270

Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 275 280 285

His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro
 290 295 300

Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu
 305 310 315 320

Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala Ala
 325 330 335

Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg
 340 345 350

Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp
 355 360 365

Leu Pro Pro Trp Thr Trp Arg Gln Gly Phe Ser Ser Leu Ala Arg Leu
370 375 380

Val Ser Asn Ser
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<210> 6
<211> 1576
<212> DNA
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<220>
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<222> (3)..(1190)

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Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg
1 5 10 15

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gct gcc cac gtc gtc tcc agg aag gga ccc ggg tcc acg agc tgc cca 95
Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro
          20           25           30

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cgt cct ctc cag gaa agg acc cg^g gtc cac gag ctg gcc acg tcc tct 143
Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser
35 40 45

gca gga agg gac ccc ggg tcc acg agc tgc cca cgt cct ctc cag gaa 191
Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu
50 55 60

ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc 239
 Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro
 65 70 75

cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc 287
 Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser
 80 85 90 95

acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct 335
 Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala
 100 105 110

gcc cac gtc ctc tcc agg agg gga cac cg_g gtt cac gag ctg ccc acg 383
 Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr
 115 120 125

ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc 431
 Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu
 130 135 140

cag gaa ggg acc cgg gtc cac gaa ctg ccc acg ccc tct cca gga ggg 479
 Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly
 145 150 155

gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly 160 165 170 175	527
tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc cgg gtc cac gaa Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu 180 185 190	575
ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro 195 200 205	623
cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu 210 215 220	671
tcc agg agg gga cac ccg gtt cac gag ctg ccc acg tcc tct cca gga Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly 225 230 235	719
ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr 240 245 250 255	767
ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser 260 265 270	815
acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala 275 280 285	863
gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg 290 295 300	911
ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala 305 310 315	959
ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala 320 325 330 335	1007
gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg 340 345 350	1055
cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu 355 360 365	1103
gac ctg ccc cca tgg acc tgg gaa cct ccc ggc tct tcc cac tcg gga Asp Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly 370 375 380	1151

aag gaa ggc tct ggg cat gga gct tta ttg agg tat agt tgacaattca 1200
 Lys Glu Gly Ser Gly His Gly Ala Leu Leu Arg Tyr Ser
 385 390 395

ggacggtgtg cactcaaggat atgcagcata acaacacctgac acacgttaggc atttgtgaaat 1260
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 tggaaagctg aggctggaga atcacttgag cctgggaggc ggaggttgcg gtgcactcca 1500
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Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro Arg
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Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala
 35 40 45

Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly
 50 55 60

Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg
 65 70 75 80

Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr
 85 90 95

Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 100 105 110

His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro
 115 120 125

Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln
 130 135 140

Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp
 145 150 155 160

Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser
 165 170 175

Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
 180 185 190
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
 195 200 205
 Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
 210 215 220
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
 225 230 235 240
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro
 245 250 255
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr
 260 265 270
 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 275 280 285
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro
 290 295 300
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu
 305 310 315 320
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala Ala
 325 330 335
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg
 340 345 350
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp
 355 360 365
 Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly Lys
 370 375 380
 Glu Gly Ser Gly His Gly Ala Leu Leu Arg Tyr Ser
 385 390 395

<210> 8
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<220>
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 1 5 10 15

gct gcc cac gtc gtc tcc agg aag gga ccc ggg tcc acg acg tgc cca Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro 20	25	30	95
cgt cct ctc cag gaa agg acc cgg gtc cac gag ctg gcc acg tcc tct Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser 35	40	45	143
gca gga agg gac ccc ggg tcc acg acg tgc cca cgt cct ctc cag gaa Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu 50	55	60	191
ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro 65	70	75	239
cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser 80	85	90	287
acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala 100	105	110	335
gcc cac gtc ctc tcc agg agg gga cac cgg gtt cac gag ctg ccc acg Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr 115	120	125	383
ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu 130	135	140	431
cag gaa ggg acc ccg gtc cac gaa ctg ccc acg ccc tct cca gga ggg Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly 145	150	155	479
gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly 160	165	170	527
tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc ccg gtc cac gaa Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu 180	185	190	575
ctg ccc acg ccg tct cca gga ggg gac acc ggg ttc acg agc tgc cca Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro 195	200	205	623
cgc cct ctc cag gaa ggg acc ccg ggt tca cga gct gcc cac gtc ctc Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu 210	215	220	671
tcc agg agg gga cac ccg gtt cac gag ctg ccc acg tcc tct cca gga Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly 225	230	235	719

ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca	767
Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr	
240 245 250 255	
ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc	815
Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser	
260 265 270	
acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct	863
Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala	
275 280 285	
gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg	911
Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg	
290 295 300	
ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc	959
Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala	
305 310 315	
ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc	1007
Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala	
320 325 330 335	
gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg	1055
Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg	
340 345 350	
cgg ccg gca gag aag ggg tcc atg atg gcg cct cgg tgc gca gcc ttg	1103
Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu	
355 360 365	
gac ctg ccc cca tgg acc tgg atg cca gtg atg cct gag gtc tgc agg	1151
Asp Leu Pro Pro Trp Thr Trp Met Pro Val Met Pro Glu Val Cys Arg	
370 375 380	
gca gtg cat acg ctc acc gcc tgg ccg ctc agg agc ctg tgc ttg acc	1199
Ala Val His Thr Leu Thr Ala Trp Pro Leu Arg Ser Leu Cys Leu Thr	
385 390 395	
ccc aaa tcc gcc ccc caa ctc cct gtt acc ggc tca ctc ctt cca	1244
Pro Lys Ser Ala Pro Gln Leu Pro Val Thr Gly Ser Leu Leu Pro	
400 405 410	
tgaggggcct tccccagggc cagccgatgc tctcctgatg gtcctgccc ttgcagatg 1304	
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tttattgagg tatagttgac aattcaggac ggtgtcact caaggtatgc agcatcacaa 1664	

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 ggtgcacacc tgggtcccc gctacttggg aagctgaggc tggagaatca cttgagcctg 1904
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 aaataaataa aggacacattt ctatcaaaa aaaaaaaaaaaaaaa 2010

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 <212> PRT
 <213> Homo sapiens

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 Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala
 35 40 45
 Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly
 50 55 60
 Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg
 65 70 75 80
 Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr
 85 90 95
 Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 100 105 110
 His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro
 115 120 125
 Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln
 130 135 140
 Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp
 145 150 155 160
 Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser
 165 170 175
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
 180 185 190
 Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
 195 200 205

Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
 210 215 220
 Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
 225 230 235 240
 Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro
 245 250 255
 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr
 260 265 270
 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 275 280 285
 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro
 290 295 300
 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu
 305 310 315 320
 Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala Ala
 325 330 335
 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg
 340 345 350
 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp
 355 360 365
 Leu Pro Pro Trp Thr Trp Met Pro Val Met Pro Glu Val Cys Arg Ala
 370 375 380
 Val His Thr Leu Thr Ala Trp Pro Leu Arg Ser Leu Cys Leu Thr Pro
 385 390 395 400
 Lys Ser Ala Pro Gln Leu Pro Val Thr Gly Ser Leu Leu Pro
 405 410

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (3)..(1349)

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 gct gcc cac gtc tcc agg aag gga ccc ggg tcc acg agc tgc cca 95
 Ala Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro
 20 25 30

cgt cct ctc cag gaa agg acc cgg gtc cac gag ctg gcc acg tcc tct		143
Arg Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser		
35	40	45
gca gga agg gac ccc ggg tcc acg agc tgc cca cgt cct ctc cag gaa		191
Ala Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu		
50	55	60
ggg acc ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc		239
Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro		
65	70	75
cgg gtc cac gag ctg ccc acg tcc tct cca gga agg gac ccc ggg tcc		287
Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser		
80	85	90
acg aac tgc cca cgt cct ctc cag gaa ggg acc ccg ggt tca cga gct		335
Thr Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala		
100	105	110
gcc cac gtc ctc tcc agg agg gga cac cgg gtt cac gag ctg ccc acg		383
Ala His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr		
115	120	125
ccc tct cca gga agg gac ccc ggg ttc atg agc tgc cca cgt cct ctc		431
Pro Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu		
130	135	140
cag gaa ggg acc cgg gtc cac gaa ctg ccc acg ccc tct cca gga ggg		479
Gln Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly		
145	150	155
gac ccg ggt cca cga gct gcc cac gtc gtc aac ggg aag gga ccc ggg		527
Asp Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly		
160	165	170
tcc acg agc tgc cca cgt cct ctc cag gaa ggg acc cgg gtc cac gaa		575
Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu		
180	185	190
ctg ccc acg cgc tct cca gga ggg gac acc ggg ttc acg agc tgc cca		623
Leu Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro		
195	200	205
cgc cct ctc cag gaa ggg acc ccc ggt tca cga gct gcc cac gtc ctc		671
Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu		
210	215	220
tcc agg agg gga cac cgg gtt cac gag ctg ccc acg tcc tct cca gga		719
Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly		
225	230	235
ggg gac acc ggg ttc acg agc tgc cca cgc cct ctc cag gag ggg aca		767
Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr		
240	245	250
		255

ccg ggt tca cga gct gcc cac gtc ctc tcc agg aag gga ccc ggg tcc 815
 Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser
 260 265 270

acg agc tgc cca cgt cct ctc cag gag ggg aca ccg ggt tca cga gct 863
 Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala
 275 280 285

gcc cac gca ctt tcc agg aag gga ccc cgg gtt cag gtc tcc tgc cgg 911
 Ala His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg
 290 295 300

ccc aca tcg tgc ctt tgt gta aat cag aag aaa gat gag gaa cag gcc 959
 Pro Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala
 305 310 315

ctc ctc tct ctc cag gca ggc ttt ggt gga ggg gct gga tct cct gcc 1007
 Leu Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala
 320 325 330 335

gca cct tcc ctg gca ggg cac cct gtg ctt gag ccc cag aac tgc agg 1055
 Ala Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg
 340 345 350

cg^g ccg gca gag aag ggg tcc atg atg gc^g cct cgg tgc gca gcc ttg 1103
 Arg Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu
 355 360 365

gac ctg ccc cca tgg acc tgg gaa cct ccc ggc tct tcc cac tcg gga 1151
 Asp Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly
 370 375 380

aag gaa ggc tct ggg cat gga ggt cg^g cca ggc ccc atc ccc gta ccc 1199
 Lys Glu Gly Ser Gly His Gly Gly Arg Pro Gly Pro Ile Pro Val Pro
 385 390 395

tgg ccc ttc ttc ctg ctt cct gtt tgt cac tgc ccc ggg gcc ttt gca 1247
 Trp Pro Phe Phe Leu Leu Pro Val Cys His Cys Pro Gly Ala Phe Ala
 400 405 410 415

cct gca ttc cct ctc tct gtg agt gtc ctg ggg ccc gtt acc cac gtc 1295
 Pro Ala Phe Pro Leu Ser Val Ser Val Leu Gly Pro Val Thr His Val
 420 425 430

acc gtc cca gga tac ctt ttc ttt tct ttc tct ctc tcc agc ttt att 1343
 Thr Val Pro Gly Tyr Leu Phe Phe Ser Phe Ser Leu Ser Ser Phe Ile
 435 440 445

gag gta tagttgacaa tt^caggacgg t^ttgactca aggtatgcag catcacaacc 1399
 Glu Val

tgacacacgt aggcatgtg aaatgagtcc cacaattggg ctaattaaca cacccatcac 1459

cttacatggt tacttcttc t^tgtggtgaga acactaaatt ttaaatagag gacacacagc 1519

ctggcaaca tagtgagacc ctgtctctac aaatataaaa aaattatctg gacgtggtgg 1579

tgcacacactg tggcccagc tacttggaa gctgaggctg gagaatcact tgagcctggg 1639

aggcggaggt tgccgtgcac tccagctgg gcgacagagg gaggccatct ctc当地ataaaataaa 1699
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<212> PRT
<213> Homo sapiens

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Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala
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Ala His Val Val Ser Arg Lys Gly Pro Gly Ser Thr Ser Cys Pro Arg
20 25 30
Pro Leu Gln Glu Arg Thr Arg Val His Glu Leu Ala Thr Ser Ser Ala
35 40 45
Gly Arg Asp Pro Gly Ser Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly
50 55 60
Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Arg
65 70 75 80
Val His Glu Leu Pro Thr Ser Ser Pro Gly Arg Asp Pro Gly Ser Thr
85 90 95
Asn Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
100 105 110
His Val Leu Ser Arg Arg Gly His Arg Val His Glu Leu Pro Thr Pro
115 120 125
Ser Pro Gly Arg Asp Pro Gly Phe Met Ser Cys Pro Arg Pro Leu Gln
130 135 140
Glu Gly Thr Arg Val His Glu Leu Pro Thr Pro Ser Pro Gly Gly Asp
145 150 155 160
Pro Gly Pro Arg Ala Ala His Val Val Asn Gly Lys Gly Pro Gly Ser
165 170 175
Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Arg Val His Glu Leu
180 185 190
Pro Thr Arg Ser Pro Gly Gly Asp Thr Gly Phe Thr Ser Cys Pro Arg
195 200 205
Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala His Val Leu Ser
210 215 220
Arg Arg Gly His Arg Val His Glu Leu Pro Thr Ser Ser Pro Gly Gly
225 230 235 240

Asp Thr Gly Phe Thr Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro
 245 250 255

 Gly Ser Arg Ala Ala His Val Leu Ser Arg Lys Gly Pro Gly Ser Thr
 260 265 270

 Ser Cys Pro Arg Pro Leu Gln Glu Gly Thr Pro Gly Ser Arg Ala Ala
 275 280 285

 His Ala Leu Ser Arg Lys Gly Pro Arg Val Gln Val Ser Cys Arg Pro
 290 295 300

 Thr Ser Cys Leu Cys Val Asn Gln Lys Lys Asp Glu Glu Gln Ala Leu
 305 310 315 320

 Leu Ser Leu Gln Ala Gly Phe Gly Gly Ala Gly Ser Pro Ala Ala
 325 330 335

 Pro Ser Leu Ala Gly His Pro Val Leu Glu Pro Gln Asn Cys Arg Arg
 340 345 350

 Pro Ala Glu Lys Gly Ser Met Met Ala Pro Arg Cys Ala Ala Leu Asp
 355 360 365

 Leu Pro Pro Trp Thr Trp Glu Pro Pro Gly Ser Ser His Ser Gly Lys
 370 375 380

 Glu Gly Ser Gly His Gly Gly Arg Pro Gly Pro Ile Pro Val Pro Trp
 385 390 395 400

 Pro Phe Phe Leu Leu Pro Val Cys His Cys Pro Gly Ala Phe Ala Pro
 405 410 415

 Ala Phe Pro Leu Ser Val Ser Val Leu Gly Pro Val Thr His Val Thr
 420 425 430

 Val Pro Gly Tyr Leu Phe Phe Ser Phe Ser Leu Ser Ser Phe Ile Glu
 435 440 445

Val

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 12
 gtagtaacag aatggacttt ga

22

<210> 13
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
agagaggaac agcatcaaag tc

22

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
caaacagggt ccaccgtgga aa

22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
gtgtttcagc cacatttcca cg

22

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
atccaccgct agaaacccac tc

22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
gaccatcaac tgatgagtgg gt

22

<210> 18
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
tcatgggggt gccttgacct tg 22

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
tggcctcaaa ggctcaaggt ca 22

<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
tgttaggacta tattgctc 18

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
cgacatttag gtgacact 18

<210> 22
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic adapter oligonucleotide

<400> 22
gtcttcacca cgggg 15

<210> 23
<211> 11
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic adapter
oligonucleotide

<400> 23
gtggtaaga c

11

<210> 24
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24
gcccttaggg agagcagc

18

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25
ccacatcgta cctttgtgt

20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 26
cactgtgtta aaacgcctgg

20

<210> 27
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 27
gttgggatta caggcacgag

20

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
cagaagcaac ccacatgacc

20

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
actacaggtt tgcaccacca

20

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
atgctctcct gatggctcct

20

<210> 31
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
aggaaatgca ggtgcaaag

19

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
actcgggaaa ggaaggctct 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
catacattga gtgcacaccg 20

<210> 34
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
gacagtcgtgc tccacatcca 20

<210> 35
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
tggagatgaa gtcttgctct tg 22

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
atatttgc tggctttggg 20

<210> 37
<211> 20

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
cccaggctgt gtgtcctcta

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20

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<210> 38
<211> 1124
<212> DNA
<213> Homo sapiens

<400> 38
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tccacgagct gggcacgtcc tctgcagggaa gggaccccggt tcacgagtc tgcccacgtc 180
ctctccagga agggaccccggt tcacgagct gtcacgacgt cctctccagg aaggaccccg 240
gggtccacga gtcacgacgt tccttcacg gaagggaccc cggtccacg aactgcccac 300
gtccttcacca ggaagggaccc cgggttcac gagctccca cgtccttcac aggaggggac 360
accgggttca cgagctcccc acgcctctc caggaaggga ccccggttc atgagctgcc 420
cacgtcctctc ccaggaaggga acgggttcc acgaactgccc cacgcctctc ccaggagggg 480
acccgggttcc acggacgtgcc cacgtcgtca acgggaaggga acccgggttcc acggacgtgcc 540
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ccacgtcctctc ccacgggggg ttcacgagct gcccacgtcc tctccaggag 720
gggacacccgg gttcacgagc tgcccacgtcc ctctccaggag gggacacccgg gttcacgag 780
ctgcccacgt ctctccaggag aaggacccgg gttcacgagc tgcccacgt cctctccaggag 840
aggggacacc gggacccgg gttcacgagc gtcacgacgt cactttccag gaagggaccc cggttcagg 900
tctcctgccc gcccacatcg tgccttgc taaatcgaaa gaaatcgatcg gaaacaggccc 960
tccttcctctc ccaggcagggc ttggggggag gggctggatc tcctggccca cttccctgg 1020
cagggcaccc tggcttgaaat cccagaact gcaggcggcc ggcagagaag gggatcgatcg 1080
tggcgctcg gtgcgcagcc ttggacctgc cccatggac ctgg 1124

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<210> 39
<211> 289
<212> DNA
<213> Homo sapiens

<400> 39
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ctgcctcaggc ctcccgaaat gttggatta caggcacgag ccactgtgcc cggccatcat 120
tccttttac tgctgactaa tagtctgctg tgtgaatcca ccgctagaaa cccactcatc 180
atgtatgtt catgtgggtt gttctgctta ttgccttatt atgaacagtg ctggataaaa 240
cgttcctgtc cactttggg catacgctca ggagtggaaac tgctgggtc 289

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<210> 40
<211> 139
<212> DNA
<213> Homo sapiens

<400> 40
gaacctcccg gctcttccca ctcggaaag gaaggctctg ggcacggagg tcggccaggc 60
cccatcccg taccctggcc cttcttcctg cttcctgttt gtcactgccc cggggccttt 120

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gcacctgcat tccctctct	139
<210> 41	
<211> 49	
<212> DNA	
<213> Homo sapiens	
<400> 41	
gaacctcccc gctcttccca ctcggaaag gaaggctctg ggcattggag	49
<210> 42	
<211> 866	
<212> DNA	
<213> Homo sapiens	
<400> 42	
atgccagtga tgcctgaggt ctgcagggca gtgcatacgc tcaccgcctg gccgctcagg 60	
agcctgtct tgacccccc caactccctg ttaccggctc actcattcca 120	
tgagggccct tccccagggc cagccgatgc ttcctgtat gtcctgtccc ttgcagatg 180	
ctgccccccgc ctgcacccat ggcctggacc ctcgcctgag cccctcagg gctctgcgcc 240	
acctaaccac aggcgtttgt tccgcaggaa ctcggcggt cttccactc gggaaaggaa 300	
ggctctggc atggaggctc gccaggcccc atcccgta cctggccctt cttctgtt 360	
cctgtttgtc actgcggccgg ggccttgca ctcgcattcc ctctctctgt gagtgtcctg 420	
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tttatttggg tatagttgac aattcaggac ggtgtgact caaggatgc agcatcacaa 540	
cctgacacac gtggcattt tgaaatgagt cccacaattt ggctaattaa cacacccatc 600	
accttacatg gttacttctt tctgtgtga gaacactaaa ttttaatag aggacacaca 660	
gcctggcaa catagtgaga ccctgtctt acaaataataaaaattatc tggacgtgg 720	
ggtgcacacc tgggttccca gctacttggg aagctgaggc tggagaatca cttgagcctg 780	
ggaggcggag gttgcgtgc actccagcct gggcgacaga gggaggccct atctcaaaa 840	
aaataataaa aggacacatt ttatc	866
<210> 43	
<211> 387	
<212> DNA	
<213> Homo sapiens	
<400> 43	
ctttatttagt gtagatgtga caattcagga cgggtgtcac tcaaggtatg cagcatcaca 60	
acctgacaca cgtaggcatt gtgaaatgag tcccacaattt gggctaatta acacacccat 120	
cacccatgtt gttacttctt ttctgtgtg agaacactaa attttaaata gaggacacac 180	
agcctggcaca acatagttag accctgtctc tacaatataaaaattatcttgcgtgg 240	
tggtcacac ctgtggtccc agctacttgg gaagctgagg ctggagaatc acttgagcct 300	
gggaggcggaa gttgcgtgtg cactccagcc tggcgacag agggaggccc tatctcaaaa 360	
taaataataaa aaggacacat ttatc	387
<210> 44	
<211> 599	
<212> DNA	
<213> Homo sapiens	
<400> 44	
gaacctcccc gctcttccca ctcggaaag gaaggctctg ggcattggagg tcggccaggc 60	
cccatccccg taccctggcc ttcttcctg ttccctgttt gtcactgccc cggggccctt 120	

gcacctgcat tcctctctc tgtgagtgtc ctggggcccg ttaccacgt caccgtcccc 180
 ggataacctt tctttcttt ctctctctcc agctttattt aggtatagtt gacaattca 240
 gacgggtgtc actcaaggta tgcagcatca caacctgaca cacgtaggca ttgtgaaatg 300
 agtcccacaa ttgggctaata taacacaccc atcaccttac atggttactt cttctgtgg 360
 tgagaacact aaattttaaa tagaggacac acagcctggg caacatagtg agaccctgtc 420
 tctacaataa taaaaaaatt atctggacgt ggtggtgac acctgtggc ccagctactt 480
 gggaaagctga ggctggagaa tcacttgac ctgggaggcg gaggttgcgg tgcactccag 540
 cctggcgcac agagggaggc cctatctcaa aataaataaa taaaggacac attcttatac 599

<210> 45
 <211> 1028
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (267)
 <223> a, t, c or g

<400> 45
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 tatagagatc ttatctactg agtagataga acgtacatga atgtacgaac agtccagacg 120
 agtaacttga ctaggataag atagacagta ccaactaatg agacaagaag agggaaatcat 180
 atagaatcat gtatctcgat tctaggcgagt gtcgacatga tcacaagcga aatacagact 240
 atgagaagag gtagaaataa taagtanact gagaagagag gtcatatgtc catacaaatc 300
 agtaaagcaa tagaaattga atacattata agccacagtt acagaattag ctaattaa 360
 caaccatggc aagcgagtta tatcaaacat agaagagtaa actctatcga ccatggtag 420
 gaacgaataa aggctcgag aagacaataa gaatgcgtgt taaacagcaa tacaagagaa 480
 tagcaccact gaagcagacc aaaggctca cccgggaagt agggaaagagg cacctcacaa 540
 ggagaggaaa gggcagtcct gatttgaaa atttcagtga aaagacagtg ttgttcccg 600
 aggcaagctt gtatcccgc atcgactctg aagaggaccc tgaggtagg ggatttttgg 660
 gcctgaccgg cctatgtga acgccaccgg ggaattcagg gagaacacacg gggccccggc 720
 ttccaggaga gcagccaggc cacagccctg aggacgggca aacccaccc aggcacgggt 780
 agaggaggc cgcccaggcc tggggctgg cggcaggggg tgaagtggac cagagccccg 840
 caaatcttaa cgtgggtgag cagtggcct gtgtggctgc gagtggtcc gtttgggc 900
 ttttgttcc tgcagcaat gatgccagcc ctgacggaaac cagtgcacgt ccaccacgag 960
 ctgcccacgt cctctccagg aagggaccgg gttccacgag ctgcccacgt cctctccagg 1020
 aagggacc 1028

<210> 46
 <211> 40
 <212> DNA
 <213> Homo sapiens

<400> 46
 actacagggtt tgcaccacca tgcctgcta atttttttt 40

<210> 47
 <211> 40
 <212> DNA
 <213> Homo sapiens

<400> 47
 actacagggtt tgcaccaccc tgcctgcta atttttttt 40

<210> 48
<211> 39
<212> DNA
<213> Homo sapiens

<400> 48
tgtgcactct tgggcatacg cctaggagtg gaactgctg 39

<210> 49
<211> 39
<212> DNA
<213> Homo sapiens

<400> 49
tgtgcactct tgggcataatg cctaggagtg gaactgctg 39

<210> 50
<211> 39
<212> DNA
<213> Homo sapiens

<400> 50
gggctctgcg ccacctaacc ccaggcgttt gttccgcag 39

<210> 51
<211> 39
<212> DNA
<213> Homo sapiens

<400> 51
gggctctgcg ccacctaacc tcaggcggtt gttccgcag 39